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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/084,546

DATE: 03/13/2002

TIME: 10:25:18

Input Set : N:\Crf3\RULE60\10084546.raw
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1 <110> APPLICANT: Cahoon, Rebecca E.
 2 <120> TITLE OF INVENTION: Vitamin B Metabolism Proteins
 3 <130> FILE REFERENCE: BB-1201-A
 4 <140> CURRENT APPLICATION NUMBER: 10/084,546
 5 <141> CURRENT FILING DATE: 2002-02-25
 6 <150> PRIOR APPLICATION NUMBER: 09/370,295
 7 <151> PRIOR FILING DATE: 1999-08-09
 8 <160> NUMBER OF SEQ ID NOS: 8
 9 <170> SOFTWARE: Microsoft Office 97
 11 <210> SEQ ID NO: 1
 12 <211> LENGTH: 1274
 13 <212> TYPE: DNA
 14 <213> ORGANISM: Zea mays
 15 <400> SEQUENCE: 1
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 17 tcaggtattg gcagcataaaa gtgttagatt tgtccttgat tgaggtaccc cttcaaagg 120
 18 caagatgttgc tggcgccgac tacgcgttat ggtatgtata atgcattctt cgagtttc 180
 19 tcttccgaaa ctgtatcaac ctgtcaacaa accagtcaag aactatgctt tagttgttct 240
 20 aaaccagcat cttccacgat tcatgcctcg actctggat catgcaaact tgaggatctg 300
 21 cgctgatgga ggagctaatac atattttga tgagatgtat cagataacca atgatgaaga 360
 22 caaaaaaaaggc accagaataa agtatgttcc agaaataatt gaaggggaca tggattctat 420
 23 aagacctgaa gtaaaaactgt tctactctag tcagggatcc aaaatttctg ataagtccaca 480
 24 taaccaggag acaacagatc tacacaaatg tatttctcgat atccatcatt gtacccctga 540
 25 tgatgaaaaaa ccaaattctt gtgtacttgt tactggagca ctaggtggaa ggtttgatca 600
 26 cgaggcggca aatatcaatg ttctgtatct gtttccggac atgaggattt tcctctatc 660
 27 agacgattgc ttgatccgac ttcttccgag aacacatcgc catgagcttt atattgagtc 720
 28 gtctgttggaa ggacccatt gtgggctttt ccctgttggaa gcaccatcaa caagcacaac 780
 29 aactactggc ctgaaatggaa atctaagtga atcaaagatg agatttggaa gcatgataag 840
 30 cacatccaac attgtgcagt cggagaaagt aactgttagaa tctgtatgcag atctttgtg 900
 31 gacaatttct ctgcgaaatc tgacataagc agttccatgt ttgttatctt ttttcttctc 960
 32 ttctctgtca agtggcaacc aagctcttgt acagccactt ttgtgtttat gagttgtgt 1020
 33 tctggtaaat aaataccatc tcatgacaaa tcgtatggat ctcatcatta gacaggatgt 1080
 34 ctaccacgat ctgtactgc tcatgacaaa tgcgtatggat acgagcaggc atgatggtt 1140
 35 tattctctt agttgtataa ctgtattgtt gtacttgca cggggtttct tgcataaaat 1200
 36 tgcattcaac agttcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaataaaaa 1260
 37 aaaaaaaaaa aaaa 1274
 39 <210> SEQ ID NO: 2
 40 <211> LENGTH: 267
 41 <212> TYPE: PRT
 42 <213> ORGANISM: Zea mays
 43 <400> SEQUENCE: 2
 44 Met Leu Trp Arg Ala Val Arg Ser Met Asp Val Ile Met His Ser Ser
 45 1 5 10 15

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46 Ser Phe Leu Leu Pro Lys Leu Tyr Gln Pro Val Asn Lys Pro Val Lys
47          20           25           30
48 Asn Tyr Ala Leu Val Val Leu Asn Gln His Leu Pro Arg Phe Met Pro
49          35           40           45
50 Arg Leu Trp Asp His Ala Asn Leu Arg Ile Cys Ala Asp Gly Gly Ala
51          50           55           60
52 Asn His Ile Phe Asp Glu Met Tyr Gln Ile Thr Asn Asp Glu Asp Lys
53          65           70           75           80
54 Lys Ser Thr Arg Asn Lys Tyr Val Pro Glu Ile Ile Glu Gly Asp Met
55          85           90           95
56 Asp Ser Ile Arg Pro Glu Val Lys Leu Phe Tyr Ser Ser Gln Gly Ser
57          100          105          110
58 Lys Ile Ser Asp Lys Ser His Asn Gln Glu Thr Thr Asp Leu His Lys
59          115          120          125
60 Cys Ile Ser Arg Ile His His Cys Thr Pro Asp Asp Glu Lys Pro Asn
61          130          135          140
62 Leu Cys Val Leu Val Thr Gly Ala Leu Gly Gly Arg Phe Asp His Glu
63          145          150          155          160
64 Ala Ala Asn Ile Asn Val Leu Tyr Leu Phe Ser Asp Met Arg Ile Val
65          165          170          175
66 Leu Leu Ser Asp Asp Cys Leu Ile Arg Leu Leu Pro Arg Thr His Arg
67          180          185          190
68 His Glu Leu Tyr Ile Glu Ser Ser Val Glu Gly Pro His Cys Gly Leu
69          195          200          205
70 Phe Pro Val Gly Ala Pro Ser Thr Ser Thr Thr Thr Gly Leu Lys
71          210          215          220
72 Trp Asn Leu Ser Glu Ser Lys Met Arg Phe Gly Ser Met Ile Ser Thr
73          225          230          235          240
74 Ser Asn Ile Val Gln Ser Glu Lys Val Thr Val Glu Ser Asp Ala Asp
75          245          250          255
76 Leu Leu Trp Thr Ile Ser Leu Arg Asn Leu Thr
77          260          265

79 <210> SEQ ID NO: 3
80 <211> LENGTH: 545
81 <212> TYPE: DNA
82 <213> ORGANISM: Zea mays
83 <400> SEQUENCE: 3
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85 agacacactc ccacgagatc catattaaga aatcggttga aggtcctcac tgtggttga 120
86 ttccgatggg tggaccgtca gctaccacaa caaccacagg gctccgatgg aatttagata 180
87 acaccaacat gatgtatgtt ggattgataa gcacatctaa catcgatggat gacgataaag 240
88 taacggtgac ttcatgttgc gatctggttt ggaccatatac gtttcggat tgagtcaac 300
89 ttgtataatt ccatgcccaa attttgtcgc ctcaaattac atgtattcag tttcaatatt 360
90 attctgttaac tggtgtgata ttgtttccg ctgcgtgtcg ttatgtccat atatgtgaac 420
91 ttattcttca tagtttagga atccagcatc tgccagccaa atgtccccac aatctatatt 480
92 cagcttttc acactttcac tgtttgtgca tctgaatatac aatcaacttt gtcgaaaaaaa 540
93 aaaaaa
95 <210> SEQ ID NO: 4
96 <211> LENGTH: 96

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97 <212> TYPE: PRT
98 <213> ORGANISM: Zea mays
99 <400> SEQUENCE: 4
100   Phe Ser Ser Ile Lys Ile Ile Leu Leu Ser Asp Asp Cys Ser Ile Phe
101       1           5           10          15
102   Leu Leu Pro Lys Thr His Ser His Glu Ile His Ile Lys Lys Ser Val
103       20          25          30
104   Glu Gly Pro His Cys Gly Leu Ile Pro Met Gly Gly Pro Ser Ala Thr
105       35          40          45
106   Thr Thr Thr Gly Leu Arg Trp Asn Leu Asp Asn Thr Asn Met Met
107       50          55          60
108   Tyr Gly Gly Leu Ile Ser Thr Ser Asn Ile Val Asp Asp Asp Lys Val
109       65          70          75          80
110   Thr Val Thr Ser Asp Ser Asp Leu Val Trp Thr Ile Ser Leu Arg Asn
111       85          90          95
113 <210> SEQ ID NO: 5
114 <211> LENGTH: 945
115 <212> TYPE: DNA
116 <213> ORGANISM: Glycine max
117 <400> SEQUENCE: 5
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119   ccttactcc acaaaggtaa actgtgcaac cgcgctcctg agaaaacaatc tgaattcctt 120
120   ccatttatca ttgaggacca cgtcggttgg a ttcattcaca aggggtttgt tgacatttg 180
121   agaggctttg ggaatgtgtt cattttcccc aaagataaat ataatggagg ctttacgga 240
122   gactttgttt ctgtcatcc aatgctaaag acagctgagg aaagaaccag tgcagttgg 300
123   tatgttagtag aacgtttggg agaggagcat attccaggaa tacggaatga gctttaccct 360
124   gtgatatatcat catttttgtc acagattttc ttttattttt aacgtgctgc agctccttat 420
125   tttggcataa aggtttatgg aacccagatg aatggctgtg ttgagctgg a tggcagaag 480
126   cacttatggaa taggaaagag aagtggtaca aaatccacat atcctggaaat gcttggatg 540
127   ctagttgcag gaggactgcc gcatggaaatc aattgtcagc agaatcttc aaaggaatgt 600
128   gaagaggaag caggaatacc tagatctatc tctgtcaacg ccataccgg tggtgcttt 660
129   tcatacaaag acattgtatgg atatagatac aagagagatg ttctgttctg ttatgatcta 720
130   aaacttccaa aagatttcat tccgaaaaat aaagatggag aagttgatag cttcaagttg 780
131   atccctgtta cacaaggtaa agaaatcata cgcaagacac agttttcaa ggcaaattgc 840
132   gctttgtaa tcattgattt cctgtttcgaa catggataca tcactcctga atatgatgg 900
133   tatttggatc tcctacgaaat ctttggatgtc cctgaaatgg 945
135 <210> SEQ ID NO: 6
136 <211> LENGTH: 314
137 <212> TYPE: PRT
138 <213> ORGANISM: Glycine max
139 <400> SEQUENCE: 6
140   Met Pro Phe Ala Tyr Leu Asn Leu Lys Leu Pro His Asn Thr Ala Gln
141       1           5           10          15
142   Leu Ile Ser Lys Pro Leu Leu His Lys Val Gln Leu Cys Asn Arg Ala
143       20          25          30
144   Pro Glu Lys Gln Ser Glu Phe Leu Pro Phe Ile Ile Glu Asp His Val
145       35          40          45
146   Val Gly Phe Ile His Lys Gly Phe Val Glu His Leu Arg Gly Phe Gly
147       50          55          60

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148 Asn Val Phe Ile Phe Pro Lys Asp Lys Tyr Asn Gly Gly Phe Tyr Gly
149      65          70          75          80
150 Asp Phe Val Ser Leu His Pro Met Leu Lys Thr Ala Glu Glu Arg Thr
151      85          90          95
152 Ser Ala Val Gly Tyr Val Val Glu Arg Leu Gly Glu Glu His Ile Pro
153      100         105         110
154 Gly Ile Arg Asn Glu Leu Tyr Pro Val Ile Ser Ser Phe Gly Ala Gln
155      115         120         125
156 Ile Phe Phe Ser Leu Glu Arg Ala Ala Pro Tyr Phe Gly Ile Lys
157      130         135         140
158 Val Tyr Gly Thr Gln Met Asn Gly Cys Val Glu Leu Asp Gly Gln Lys
159      145         150         155         160
160 His Leu Trp Ile Gly Lys Arg Ser Gly Thr Lys Ser Thr Tyr Pro Gly
161      165         170         175
162 Met Leu Asp Glu Leu Val Ala Gly Gly Leu Pro His Gly Ile Asn Cys
163      180         185         190
164 Gln Gln Asn Leu Ala Lys Glu Cys Glu Glu Ala Gly Ile Pro Arg
165      195         200         205
166 Ser Ile Ser Val Asn Ala Ile Pro Val Gly Ala Val Ser Tyr Lys Asp
167      210         215         220
168 Ile Asp Gly Tyr Arg Tyr Lys Arg Asp Val Leu Phe Cys Tyr Asp Leu
169      225         230         235         240
170 Lys Leu Pro Lys Asp Phe Ile Pro Lys Asn Lys Asp Gly Glu Val Asp
171      245         250         255
172 Ser Phe Lys Leu Ile Pro Val Thr Gln Val Ala Glu Ile Ile Arg Lys
173      260         265         270
174 Thr Gln Phe Phe Lys Ala Asn Cys Ala Leu Val Ile Ile Asp Phe Leu
175      275         280         285
176 Phe Arg His Gly Tyr Ile Thr Pro Glu Tyr Asp Gly Tyr Leu Asp Leu
177      290         295         300
178 Leu Arg Ser Leu Arg Ile Gly Asp Cys Ser
179      305         310

181 <210> SEQ ID NO: 7
182 <211> LENGTH: 1406
183 <212> TYPE: DNA
184 <213> ORGANISM: Glycine max
185 <400> SEQUENCE: 7
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188 ttccgtttct ctaaaatgtacg ctctcggtgt tctcaaccaa agcctcccgaa gatttgctcc 180
189 cctgtttgg gaccacgctc aagtgcgagt ttgtgctgat ggagggtccca atagggtgtta 240
190 tggatggaaatgtt cctctttctt tccctcatca acaaccttcc catgttcgca ccaggtacaa 300
191 gcctgtatgtt attaaagggg acatggattt aatcaggaca gaagtacttg acttctatgc 360
192 aaagctggga actaagataa ttgtatggatc tcattatgtac gacaccacag atttacacaa 420
193 atgtgtggca tacatacgta acctcacccc aaatattgtat ggagcagaac tatgcattct 480
194 tggatggatgtt gcaacttgggtt ggagatttgc ccatgagattt gggaaatatttta acgtgtgtt 540
195 ccgatttcc aacacacgaa ttatccttctt atctgtatgtat tgcctcatttcc accttcttcc 600
196 aaagaatcat tgcataaaaa tctttgttca atcttctgtt gagggtccgc atttgtgtgtt 660
197 cattccccattt gggatgccgtt ctggaaagctc tacaaccaca ggactcaaat gggacctcaa 720

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198	tgatgcagcg atgagtttg gaggttaat aagcacatca aatattgtaa aaggggaaat	780
199	agtacagta cagtctgatt cagatcttct ttggactatt tctattaaga agctctagga	840
200	tttacatgtt gcacagtgc cgttgcatttcc agatcttga taccaattta tatgggtctt	900
201	gttccattta aaggccagag ctctgtctga ccttttttta tggttcattc ttcaattta	960
202	ctctgtgaat tgtgggaggg tggaaaggaa tttagggagtt attcttaat atagaagtt	1020
203	cagtttcaa agaggttact tacattcctt ggatcagttg cattgtatgt tattgttac	1080
204	cgtaaatgaa atagcagaat aagatggcaa aaaacaaaaa cagaaattta aagaaggaga	1140
205	aaatcatgtc atgtacttatt ttgcttatgc atacagagca atggactgtt agttgccgt	1200
206	ctactctgtg gttcgggacc attaccacaa caggtcaattt attctggta atttctatgt	1260
207	gatatggat tttcaattta gaagaatgag aaattattat gtgtgagacg ggctttgtaa	1320
208	tttacaagaa cgagttaata aaattttattt atgcatgagt ttgaatgcaa aaaaaaaaaa	1380
209	aaaaaaaaaaa aaaaaaaaaaaa aaaaaaa	1406
211 <210>	SEQ ID NO: 8	
212 <211>	LENGTH: 259	
213 <212>	TYPE: PRT	
214 <213>	ORGANISM: Glycine max	
215 <400>	SEQUENCE: 8	
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218	Pro Asn Thr Thr Cys Ser Leu Ser Leu Lys Tyr Ala Leu Val Val Leu	
219	20 25 30	
220	Asn Gln Ser Leu Pro Arg Phe Ala Pro Leu Leu Trp Asp His Ala Gln	
221	35 40 45	
222	Val Arg Val Cys Ala Asp Gly Gly Ala Asn Arg Val Tyr Asp Glu Met	
223	50 55 60	
224	Pro Leu Phe Phe Pro His Gln Gln Pro Ser His Val Arg Thr Arg Tyr	
225	65 70 75 80	
226	Lys Pro Asp Val Ile Lys Gly Asp Met Asp Ser Ile Arg Thr Glu Val	
227	85 90 95	
228	Leu Asp Phe Tyr Ala Lys Leu Gly Thr Lys Ile Ile Asp Glu Ser His	
229	100 105 110	
230	Asp Gln Asp Thr Thr Asp Leu His Lys Cys Val Ala Tyr Ile Arg Asp	
231	115 120 125	
232	Leu Thr Pro Asn Ile Asp Gly Ala Glu Leu Cys Ile Leu Val Ala Gly	
233	130 135 140	
234	Ala Leu Gly Gly Arg Phe Asp His Glu Ile Gly Asn Ile Asn Val Leu	
235	145 150 155 160	
236	Cys Arg Phe Ser Asn Thr Arg Ile Ile Leu Leu Ser Asp Asp Cys Leu	
237	165 170 175	
238	Ile His Leu Leu Pro Lys Asn His Cys His Lys Ile Phe Val Gln Ser	
239	180 185 190	
240	Ser Val Glu Gly Pro His Cys Gly Val Ile Pro Ile Gly Met Pro Ser	
241	195 200 205	
242	Gly Ser Ser Thr Thr Gly Leu Lys Trp Asp Leu Asn Asp Ala Ala	
243	210 215 220	
244	Met Ser Phe Gly Gly Leu Ile Ser Thr Ser Asn Ile Val Lys Gly Glu	
245	225 230 235 240	
246	Ile Val Thr Val Gln Ser Asp Ser Asp Leu Leu Trp Thr Ile Ser Ile	
247	245 250 255	

VERIFICATION SUMMARY

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